This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims

1. (currently amended) A nucleic acid primer comprising an oligonucleotide that selectively hybridizes to a highly conserved region of a nucleic acid molecule of HIV-1 between nucleotide positions 4550 and 5126 or 7746 and 8459 of the HXB2 strain, wherein the oligonucleotide does not selectively hybridize to a region of the HXB2 strain between 4754-4984.

2. (original) The primer of Claim 1 wherein the oligonucleotide hybridizes to a region of the *env* gene of HIV-1 between nucleotide positions selected from the group consisting of 7746 to 7772; 7817 to 7844; 8220 to 8258; 8432 to 8459; 7789 to 7816; 8347 to 8374; 7850 to 7879; 8265 to 8294; and 8281 to 8310.

3. (currently amended) The primer of Claim 1 wherein the oligonucleotide hybridizes to a region of the *pol* gene of HIV-1 between nucleotide positions selected from the group consisting of 4550 to 4625; 4626 to 4753; ~~4754 to 4984;~~ 4985 to 5126; 4596 to 4625; 4724 to 4753; ~~4956 to 4984;~~ and 5051 to 5080.

4. (original) The primer of Claim 1 having a length of 18-40 nucleotides.

5. (currently amended) The primer of Claim 1 wherein the oligonucleotide has a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID

NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, ~~SEQ ID NO:9, and conservative substitutions thereof~~.

6. (currently amended) A method of detecting HIV-1 groups M, N and O and SIVcpz in a biological sample comprising

combining the sample with a first primer under selective hybridization conditions for the selective hybridization of the first primer to HIV-1 nucleic acids in the sample, wherein the first primer comprises an oligonucleotide that selectively hybridizes to a highly conserved region of the nucleic acid molecule of HIV-1 between nucleotide positions 4550 and 5126 or 7746 and 8459 of the HXB2 strain, wherein the oligonucleotide does not selectively hybridize to a region of the HXB2 strain between 4754-4984; and

detecting hybridization of the primer to HIV-1 nucleic acids,

wherein detection of hybridization of the primer to HIV-1 nucleic acids indicates the presence of HIV-1 in the sample.

7. (original) The method of Claim 6 wherein the first primer hybridizes to a first region of the *env* gene of HIV-1 between nucleotide positions selected from the group consisting of HIV-1 between nucleotide positions selected from the group consisting of 7746 to 7772; 7817 to 7844; 8220 to 8258; 8432 to 8459; 7789 to 7816; 8347 to 8374; 7850 to 7879; 8265 to 8294; and 8281 to 8310.

8. (currently amended) The method of Claim 6 wherein the first primer hybridizes to a first region of the *pol* gene of HIV-1 between nucleotide positions selected from the group consisting

4550 to 4625; 4626 to 4753; ~~4754 to 4984;~~ 4596 to 4625; 4724 to 4753; and ~~4956 to 4984;~~ and 8265 to 8294.

9. (currently amended) The method of Claim 6 wherein the oligonucleotide has a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, ~~SEQ ID NO:9, and conservative substitutions thereof.~~

10. (currently amended) The method of Claim 6 further comprising the step of combining the sample with a second primer under selective hybridization conditions for the selective hybridization of the second primer to HIV-1 nucleic acids in the sample, wherein the second primer comprises an oligonucleotide that selectively hybridizes to a second highly conserved region of the nucleic acid molecule of HIV-1 between nucleotide positions 4550 and 5126 or 7746 and 8459 of the HXB2 strain wherein the oligonucleotide does not selectively hybridize to a region of the HXB2 strain between 4754-4984, wherein the first and second primers are a first primer pair, and wherein the primer pair and the sample are incubated under nucleic acid amplification conditions to amplify HIV-1 nucleic acids in the sample.

11. (original) The method of Claim 10 wherein the second primer hybridizes to a second region of the *env* gene of HIV-1 between nucleotide positions selected from the group consisting of 7746 to 7772; 7817 to 7844; 8220 to 8258; 8432 to 8459; 7789 to 7816; 8347 to 8374; 7850 to 7879; 8265 to 8294; and 8281 to 8310.

12. (currently amended) The method of Claim 10 wherein the second primer hybridizes to a second region of the *pol* gene of HIV-1 between nucleotide positions selected from the group consisting of 4550 to 4625; 4626 to 4753; ~~4754 to 4954;~~ ~~4885 to 5126;~~ 4985-5126, 4596 to 4625; 4724 to 4753; ~~4956 to 4984;~~ and 5051 to 5080.

13. (currently amended) The method of Claim 10 wherein the second primer has a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, ~~SEQ ID NO:9, and conservative substitutions thereof~~.

14. (original) The method of Claim 10 wherein the first primer pair comprises a forward primer and a reverse primer, wherein the forward primer comprises the nucleotide sequence of SEQ ID NO:1 and the reverse primer comprises the nucleotide sequence of SEQ ID NO:2, or wherein the forward primer comprises the nucleotide sequence of SEQ ID NO:6 and the reverse primer comprises the nucleotide sequence of SEQ ID NO:7.

15. (original) The method of Claim 10 further comprising a second primer pair, wherein the first and second primer pairs are nested.

16. (original) The method of Claim 15 wherein the second primer pair comprises a forward primer and a reverse primer, wherein the forward primer comprises the nucleotide sequence of SEQ ID NO:3 and the reverse primer comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:4 and SEQ ID NO:5, or wherein the forward primer comprises the

nucleotide sequence of SEQ ID NO:8 and the reverse primer comprises the nucleotide sequence of SEQ ID NO:9.

17. (currently amended) A method for detecting HIV-1 group N or chimpanzee SIV in a biological sample comprising

combining the sample with a first primer under selective hybridization conditions for the selective hybridization of the first primer to HIV-1 or chimpanzee SIV nucleic acids in the sample, wherein the first primer comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7[[;]] and SEQ ID NO:8, ~~and SEQ ID NO:9~~ and

detecting hybridization of the primer to HIV-1 or chimpanzee SIV nucleic acids,

wherein detection of hybridization of the primer to HIV-1 or chimpanzee SIV nucleic acids indicates the presence of HIV-1 or chimpanzee SIV in the sample.

18. (currently amended) The method of Claim 17 further comprising a second primer that hybridizes to a second highly conserved region of the nucleic acid molecule between nucleotide positions 4450 and 5126 or 7746 and 8459 of the HXB2 strain of HIV-1, wherein the oligonucleotide does not selectively hybridize to a region of the HXB2 strain between 4754-4984, wherein the first and second primers are a primer pair, and wherein the primer pair and the sample are incubated under nucleic acid amplification conditions to amplify HIV-1 nucleic acids in the sample.

19. (currently amended) The method of Claim 18 wherein the second primer has a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7[[,]] and SEQ ID NO:8, ~~SEQ ID NO:9, and conservative substitutions thereof~~.

20. (new) The primer of Claim 1, wherein amplification occurs under amplification conditions comprising 30-40 cycles of heating at 93-97°C for 30-90 seconds, at 45-57°C for 30-90 seconds, and at 70-74°C for 30-90 seconds.

21. (new) The method of Claim 6, wherein amplification occurs under amplification conditions comprising 30-40 cycles of heating at 93-97°C for 30-90 seconds, at 45-57°C for 30-90 seconds, and at 70-74°C for 30-90 seconds.